



#4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tryggvason, Karl
Kallunki, Pekka
Pyke, Charles

(ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
(B) STREET: 1100 Superior Ave, Suite 700
(C) CITY: Cleveland
(D) STATE: Ohio
(E) COUNTRY: USA
(F) ZIP: 44114

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unknown
(B) FILING DATE: 08 January 2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/663,147
(B) FILING DATE: 150-September 2000
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Minnich, Richard, J.
(B) REGISTRATION NUMBER: 24,175
(C) REFERENCE/DOCKET NUMBER: TRV 20014

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 216-861-5582
(B) TELEFAX: 216-241-1666

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTCACCAA GACTTACACA

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATCACTGA GCAGCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTACCAGA ACCGAGTTCG

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTACCA GGCTTGAGAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTACTGCGGA ATCTCACAGC

20



(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACACTGTTC AACCCAGGGT

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACAAGCCC TCTCACTGGT

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGAGACTG TGCTGATAAG

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATACCTCTC TACATGGCAT

20



(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGTCTCGCTG AATCTCTCTT

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTACAACTAG CATGGTGCC

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..183

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..3699

(ix) FEATURE:

- (A) NAME/KEY: polyA_site
- (B) LOCATION: 4433

(ix) FEATURE:

- (A) NAME/KEY: polyA_site
- (B) LOCATION: 5195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG	60
AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	165
1 5 10 15	
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	213
20 25 30	
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly	261
35 40 45	
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His	309
50 55 60	
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg	357
65 70 75 80	
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys	405
85 90 95	
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg	453
100 105 110	
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys	501
115 120 125	
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala	549
130 135 140	
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala	597
145 150 155 160	
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu	645
165 170 175	
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His	693
180 185 190	
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr	741
195 200 205	
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	789

210	215	220	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe 225 230 235 240			837
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys 245 250 255			885
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp 260 265 270			933
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile 275 280 285			981
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly 290 295 300			1029
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn 305 310 315 320			1077
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr 325 330 335			1125
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr 340 345 350			1173
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala 355 360 365			1221
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys 370 375 380			1269
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr 385 390 395 400			1317
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys 405 410 415			1365
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr 420 425 430			1413
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly 435 440 445			1461
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT			1509

Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	
450						455					460					
CAT	AAC	GGG	TTC	AGC	TGC	TCA	GTG	ATT	CCG	GAG	ACG	GAG	GAG	GTG	GTG	1557
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val	
465						470				475					480	
TGC	AAT	AAC	TGC	CCT	CCC	GGG	GTC	ACC	GGT	GCC	CGC	TGT	GAG	CTC	TGT	1605
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	
						485			490				495			
GCT	GAT	GGC	TAC	TTT	GGG	GAC	CCC	TTT	GGT	GAA	CAT	GGC	CCA	GTG	AGG	1653
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	
						500			505				510			
CCT	TGT	CAG	CCC	TGT	CAA	TGC	AAC	AGC	AAT	GTG	GAC	CCC	AGT	GCC	TCT	1701
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser	
						515			520				525			
GGG	AAT	TGT	GAC	CGG	CTG	ACA	GGC	AGG	TGT	TTG	AAG	TGT	ATC	CAC	AAC	1749
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	
						530			535				540			
ACA	GCC	GGC	ATC	TAC	TGC	GAC	CAG	TGC	AAA	GCA	GGC	TAC	TTC	GGG	GAC	1797
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	
						545			550				555			560
CCA	TTG	GCT	CCC	AAC	CCA	GCA	GAC	AAG	TGT	CGA	GCT	TGC	AAC	TGT	AAC	1845
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	
						565			570				575			
CCC	ATG	GGC	TCA	GAG	CCT	GTA	GGG	TGT	CGA	AGT	GAT	GGC	ACC	TGT	GTT	1893
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val	
						580			585				590			
TGC	AAG	CCA	GGG	TTT	GGT	GGC	CCC	AAC	TGT	GAG	CAT	GGA	GCA	TTC	AGC	1941
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser	
						595			600				605			
TGT	CCA	GCT	TGC	TAT	AAT	CAA	GTG	AAG	ATT	CAG	ATG	GAT	CAG	TTT	ATG	1989
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met	
						610			615				620			
CAG	CAG	CTT	CAG	AGA	ATG	GAG	GCC	CTG	ATT	TCA	AAG	GCT	CAG	GGT	GGT	2037
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly	
						625			630				635			640
GAT	GGA	GTA	GTA	CCT	GAT	ACA	GAG	CTG	GAA	GGC	AGG	ATG	CAG	CAG	GCT	2085
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Gly	Arg	Met	Gln	Gln	Ala		
						645			650				655			
GAG	CAG	GCC	CTT	CAG	GAC	ATT	CTG	AGA	GAT	GCC	CAG	ATT	TCA	GAA	GGT	2133
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly	
						660			665				670			
GCT	AGC	AGA	TCC	CTT	GGT	CTC	CAG	TTG	GCC	AAG	GTG	AGG	AGC	CAA	GAG	2181
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu	
						675			680				685			

AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg 690 695 700	2229
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His 705 710 715 720	2277
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser 725 730 735	2325
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn 740 745 750	2373
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His 755 760 765	2421
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp 770 775 780	2469
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly 785 790 795 800	2517
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT Val Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu 805 810 815	2565
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg 820 825 830	2613
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser 835 840 845	2661
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln 850 855 860	2709
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA Ser Phe Gln Val Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser 865 870 875 880	2757
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln 885 890 895	2805
AAG AAT CTG GGA AAC TGG AAA GAA GAA GCA CAG CAG CTC TTA CAG AAT Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn 900 905 910	2853
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	2901

915	920	925	
CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr 930 935 940			2949
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu 945 950 955 960			2997
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu 965 970 975			3045
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln 980 985 990			3093
GCA GAA AGA GCC CTG GGG AGC GCT GCT GAT GCA CAG AGG GCA AAG Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys 995 1000 1005			3141
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu 1010 1015 1020			3189
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu 1025 1030 1035 1040			3237
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val 1045 1050 1055			3285
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp 1060 1065 1070			3333
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala 1075 1080 1085			3381
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly 1090 1095 1100			3429
CTC CTG CAT CTG ATG GAC CAG CCT CTC AGT GTA GAT GAA GAG GGG CTG Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu 1105 1110 1115 1120			3477
GTC TTA CTG GAG CAG AAG CTT TCC CGA GCC AAG ACC CAG ATC AAC AGC Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser 1125 1130 1135			3525
CAA CTG CGG CCC ATG ATG TCA GAG CTG GAA GAG AGG GCA CGT CAG CAG Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln 1140 1145 1150			3573

AGG GGC CAC CTC CAT TTG CTG GAG ACA AGC ATA GAT GGG ATT CTG GCT Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala 1155 1160 1165	3621
GAT GTG AAG AAC TTG GAG AAC ATT AGG GAC AAC CTG CCC CCA GGC TGC Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys 1170 1175 1180	3669
TAC AAT ACC CAG GCT CTT GAG CAA CAG TGA AGCTGCCATA AATATTTCTC Tyr Asn Thr Gln Ala Leu Glu Gln Gln *1185 1190	3719
AACTGAGGTT CTTGGGATAC AGATCTCAGG GCTCGGGAGC CATGTCATGT GAGTGGTGG GATGGGGACA TTTGAACATG TTTAATGGGT ATGCTCAGGT CAACTGACCT GACCCCATTC CTGATCCCCT GGCCAGGTGG TTGTCCTTATT GCACCATACT CCTTGCTTCC TGATGCTGGG CATGAGGCAG ATAGGCACTG GTGTGAGAAT GATCAAGGAT CTGGACCCCA AAGATAGACT GGATGGAAAG ACAAACTGCA CAGGCAGATG TTTGCCTCAT AATAGTCGTA AGTGGAGTCC TGGAAATTGG ACAAGTGCTG TTGGGATATA GTCAACTTAT TCTTGAGTA ATGTGACTAA AGGAAAAAAC TTTGACTTTG CCCAGGCATG AAATTCTTCC TAATGTCAGA ACAGAGTGCA ACCCAGTCAC ACTGTGGCCA GTAAAATACT ATTGCCTCAT ATTGTCCTCT GCAAGCTTCT TGCTGATCAG AGTTCCCTCCT ACTTACAACC CAGGGTGTGA ACATGTTCTC CATTTCAG CTGGAAGAAG TGAGCAGTGT TGGAGTGAGG ACCTGTAAGG CAGGCCATT CAGAGCTATG GTGCTTGCTG GTGCCTGCCA CCTTCAAGTT CTGGACCTGG GCATGACATC CTTCTTTA ATGATGCCAT GGCAACTTAG AGATTGCATT TTTATTAAAG CATTTCCTAC CAGCAAAGCA AATGTTGGGA AAGTATTAC TTTTCGGTT TCAAAGTGAT AGAAAAGTGT GGCTTGGCA TTGAAAGAGG TAAAATTCTC TAGATTATT AGTCCTAATT CAATCCTACT TTTCGAACAC CAAAAATGAT GCGCATCAAT GTATTTATC TTATTTCTC AATCTCCTCT CTCTTCCCTC CACCCATAAT AAGAGAATGT TCCTACTCAC ACTTCAGCTG GGTACACATCC ATCCCTCCAT TCATCCTTCC ATCCATCTT CCATCCATTA CCTCCATCCA TCCTTCCAAC ATATATTTAT TGAGTACCTA CTGTGTGCCA GGGGCTGGTG GGACAGTGGT GACATAGTCT CTGCCCTCAT AGAGTTGATT GTCTAGTGAG GAAGACAAGC ATTTTAAAAA AATAAATTAA AACTTACAAA CTTGTGTTGT CACAAGTGGT GTTTATTGCA ATAACCGCTT GGTTGCAAC CTCTTGCTC AACAGAACAT ATGTTGCAAG ACCCTCCCAT GGGCACTGAG TTTGGCAAGG ATGACAGAGC TCTGGGTTGT GCACATTCT TTGCATTCCA GCGTCACTCT GTGCCTCTA CAACTGATTG CAACAGACTG TTGAGTTATG ATAACACCAG TGGGAATTGC TGGAGGAACC AGAGGCACCT CCACCTTGGC TGGGAAGACT ATGGTGCTGC CTTGCTTCTG TATTCCTTG GATTTCCCTG	3779 3839 3899 3959 4019 4079 4139 4199 4259 4319 4379 4439 4499 4559 4619 4679 4739 4799 4859 4919 4979 5039 5099 5159

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Ala	Leu	Trp	Leu	Gly	Cys	Cys	Leu	Cys	Phe	Ser	Leu	Leu	Leu
1					5				10					15	

Pro	Ala	Ala	Arg	Ala	Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly
					20			25					30		

Lys	Ser	Arg	Gln	Cys	Ile	Phe	Asp	Arg	Glu	Leu	His	Arg	Gln	Thr	Gly
					35			40				45			

Asn	Gly	Phe	Arg	Cys	Leu	Asn	Cys	Asn	Asp	Asn	Thr	Asp	Gly	Ile	His
					50			55			60				

Cys	Glu	Lys	Cys	Lys	Asn	Gly	Phe	Tyr	Arg	His	Arg	Glu	Arg	Asp	Arg
					65			70			75		80		

Cys	Leu	Pro	Cys	Asn	Cys	Asn	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Arg	Cys
					85			90			95				

Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg
					100			105			110				

Cys	Asp	Arg	Cys	Leu	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys
					115			120			125				

Thr	Gln	Asp	Gln	Arg	Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala
					130			135			140				

Gly	Ile	Ala	Gly	Pro	Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala
					145			150			155		160		

Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Ser	Gly	Tyr	Tyr	Asn	Leu
					165			170			175				

Asp	Gly	Gly	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His
					180			185			190				

Ser	Ala	Ser	Cys	Arg	Ser	Ser	Ala	Glu	Tyr	Ser	Val	His	Lys	Ile	Thr
					195			200			205				

Ser	Thr	Phe	His	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn
					210			215			220				

Gly	Ser	Pro	Ala	Lys	Leu	Gln	Trp	Ser	Gln	Arg	His	Gln	Asp	Val	Phe
					225			230			235		240		

Ser	Ser	Ala	Gln	Arg	Leu	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	245	250	255
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp			
260	265	270	
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile			
275	280	285	
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly			
290	295	300	
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn			
305	310	315	320
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr			
325	330	335	
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr			
340	345	350	
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala			
355	360	365	
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys			
370	375	380	
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr			
385	390	395	400
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys			
405	410	415	
Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr			
420	425	430	
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly			
435	440	445	
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys			
450	455	460	
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val			
465	470	475	480
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys			
485	490	495	
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg			
500	505	510	
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser			
515	520	525	
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn			
530	535	540	
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp			
545	550	555	560
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn			

565

570

575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln

885	890	895
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn		
900	905	910
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn		
915	920	925
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr		
930	935	940
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu		
945	950	955
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu		
965	970	975
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln		
980	985	990
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys		
995	1000	1005
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu		
1010	1015	1020
Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu		
1025	1030	1035
Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val		
1045	1050	1055
Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp		
1060	1065	1070
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala		
1075	1080	1085
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly		
1090	1095	1100
Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu		
1105	1110	1115
Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser		
1125	1130	1135
Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln		
1140	1145	1150
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala		
1155	1160	1165
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys		
1170	1175	1180
Tyr Asn Thr Gln Ala Leu Glu Gln Gln		
1185	1190	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..183

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..3453

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 4021..4316
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "HUMAN ALU"

(ix) FEATURE:

- (A) NAME/KEY: polyA_site
- (B) LOCATION: 4296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACCACCTGA	TCGAAGGAAA	AGGAAGGCAC	AGCGGAGCGC	AGAGTGAGAA	CCACCAACCG	60
AGGCGCCGGG	CAGCGACCCC	TGCAGCGGAG	ACAGAGACTG	AGCGGCCCGG	CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG						165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu						
1195	1200		1205		1210	
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG						213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly						
1215	1220		1225			
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT						261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly						
1230	1235		1240			
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC						309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His						
1245	1250		1255			
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC						357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg						
1260	1265		1270			
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT						405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys						
1275	1280		1285		1290	
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA						453

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg			
1295	1300	1305	
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC			501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys			
1310	1315	1320	
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT			549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala			
1325	1330	1335	
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT			597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala			
1340	1345	1350	
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG			645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu			
1355	1360	1365	1370
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT			693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His			
1375	1380	1385	
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC			741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr			
1390	1395	1400	
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT			789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn			
1405	1410	1415	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT			837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe			
1420	1425	1430	
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA			885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys			
1435	1440	1445	1450
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC			933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp			
1455	1460	1465	
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC			981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile			
1470	1475	1480	
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC			1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly			
1485	1490	1495	
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT			1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn			
1500	1505	1510	
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT			1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr			
1515	1520	1525	1530
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT			1173

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr			
1535	1540	1545	
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC			1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala			
1550	1555	1560	
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT			1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys			
1565	1570	1575	
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC			1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr			
1580	1585	1590	
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT			1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys			
1595	1600	1605	1610
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT			1413
Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr			
1615	1620	1625	
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT			1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly			
1630	1635	1640	
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT			1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys			
1645	1650	1655	
CAT AAC GGG TTC AGC TGC TCA GTG ATT CCG GAG ACG GAG GAG GTG GTG			1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val			
1660	1665	1670	
TGC AAT AAC TGC CCT CCC GGG GTC ACC GGT GCC CGC TGT GAG CTC TGT			1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys			
1675	1680	1685	1690
GCT GAT GGC TAC TTT GGG GAC CCC TTT GGT GAA CAT GGC CCA GTG AGG			1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg			
1695	1700	1705	
CCT TGT CAG CCC TGT CAA TGC AAC AGC AAT GTG GAC CCC AGT GCC TCT			1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser			
1710	1715	1720	
GGG AAT TGT GAC CGG CTG ACA GGC AGG TGT TTG AAG TGT ATC CAC AAC			1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn			
1725	1730	1735	
ACA GCC GGC ATC TAC TGC GAC CAG TGC AAA GCA GGC TAC TTC GGG GAC			1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp			
1740	1745	1750	
CCA TTG GCT CCC AAC CCA GCA GAC AAG TGT CGA GCT TGC AAC TGT AAC			1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn			
1755	1760	1765	1770
CCC ATG GGC TCA GAG CCT GTA GGA TGT CGA AGT GAT GGC ACC TGT GTT			1893

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val		
1775	1780	1785
TGC AAG CCA GGA TTT GGT GGC CCC AAC TGT GAG CAT GGA GCA TTC AGC		1941
Cys Lys Pro Gly Phe Gly Pro Asn Cys Glu His Gly Ala Phe Ser		
1790	1795	1800
TGT CCA GCT TGC TAT AAT CAA GTG AAG ATT CAG ATG GAT CAG TTT ATG		1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met		
1805	1810	1815
CAG CAG CTT CAG AGA ATG GAG GCC CTG ATT TCA AAG GCT CAG GGT GGT		2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly		
1820	1825	1830
GAT GGA GTA GTA CCT GAT ACA GAG CTG GAA GGC AGG ATG CAG CAG GCT		2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala		
1835	1840	1845
1850		
GAG CAG GCC CTT CAG GAC ATT CTG AGA GAT GCC CAG ATT TCA GAA GGT		2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly		
1855	1860	1865
GCT AGC AGA TCC CTT GGT CTC CAG TTG GCC AAG GTG AGG AGC CAA GAG		2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu		
1870	1875	1880
AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA		2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg		
1885	1890	1895
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC		2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His		
1900	1905	1910
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC		2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser		
1915	1920	1925
1930		
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT		2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn		
1935	1940	1945
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC		2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His		
1950	1955	1960
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC		2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp		
1965	1970	1975
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA		2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly		
1980	1985	1990
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT		2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu		
1995	2000	2005
2010		
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG		2613

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg	2015	2020	2025	
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser	2030	2035	2040	2661
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln	2045	2050	2055	2709
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser	2060	2065	2070	2757
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln	2075	2080	2085	2805
AAG AAT CTG GGA AAC TGG AAA GAA GCA CAG CAG CTC TTA CAG AAT Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn	2095	2100	2105	2853
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	2110	2115	2120	2901
CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr	2125	2130	2135	2949
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu	2140	2145	2150	2997
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu	2155	2160	2165	3045
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln	2175	2180	2185	3093
GCA GAA AGA GCC CTG GGG AGC GCT GCT GAT GCA CAG AGG GCA AAG Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys	2190	2195	2200	3141
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu	2205	2210	2215	3189
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu	2220	2225	2230	3237
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val	2235	2240	2245	3285
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT				3333

Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp	
2255							2260							2265		
GCA	GTA	CAG	ATG	GTG	ATT	ACA	GAA	GCC	CAG	AAG	GTT	GAT	ACC	AGA	GCC	3381
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala	
2270							2275							2280		
AAG	AAC	GCT	GGG	GTT	ACA	ATC	CAA	GAC	ACA	CTC	AAC	ACA	TTA	GAC	GGC	3429
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly	
2285							2290							2295		
CTC	CTG	CAT	CTG	ATG	GGT	ATG	TGA	ACCCACAACC	CACAACCTTC	CAGCTCCATG						3483
Leu	Leu	His	Leu	Met	Gly	Met	*									
2300							2305									
CTCCAGGGCT	TTGCTCCAGA	ACACTCACTA	TACCTAGCCC	CAGCAAAGGG	GAGTCTCAGC											3543
TTTCCTTAAG	GATATCAGTA	AATGTGCTTT	GTTTCCAGGC	CCAGATAACT	TTCGGCAGGT											3603
TCCCTTACAT	TTACTGGACC	CTGTTTACC	GTTGCTAAGA	TGGGTCACTG	AACACCTATT											3663
GCACCTGGGG	GTAAAGGTCT	GTGGGCCAAA	GAACAGGTGT	ATATAAGCAA	CTTCACAGAA											3723
CACGAGACAG	CTTGGGAATC	CTGCTAAAGA	GTCTGGCCTG	GACCCTGAGA	AGCCAGTGGA											3783
CAGTTTAAG	CAGAGGAATA	ACATCACCAC	TGTATATTTC	AGAAAGATCA	CTAGGGCAGC											3843
CGAGTGGAGG	AAAGCTTGAA	GAGGGGGTTA	GAGAGAAGGC	AGGTTGAGAC	TACTTAAGAT											3903
ATTGTTGAAA	TAATTGAAGA	GAGAAATGAC	AGGAGCCTGC	TCTAAGGCAG	TAGAATGGTG											3963
GCTGGGAAGA	TGTGAAGGAA	GATTTCCC	GTCTGTGAAG	TCAAGAATCA	CTTGCCGGCC											4023
GGGTGTGGTG	GCTCACGCCT	GTAATTCTAG	CACTTTGGGA	GACTGAAGCG	GGTGGATCAC											4083
CCGAGGTCAG	GAGTTGAAGA	CCAGCCTGGC	CAACATGGTG	AAACCCCTGTC	TCTACTAAAA											4143
GTACAAAAAT	TAGCTGGATG	ATGGTGGTGG	GCGCCTGTAA	TTCCAGCTAC	TCAGGAGTCT											4203
GAGGCAGGAG	AATCGCTTGA	ACCCAGGAGG	CGAGGTTACA	GTGAGCCAAG	ATTGCACCAC											4263
TGCTCTTCCA	GCCTGGGAAC	AGAGAGACTG	CCTAAAAAAA	AAAAAAA	AAA											4316

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Pro	Ala	Leu	Trp	Leu	Gly	Cys	Cys	Leu	Cys	Phe	Ser	Leu	Leu	Leu
1				5					10				15		
Pro	Ala	Ala	Arg	Ala	Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly
									25				30		

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
35 40 45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
50 55 60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65 70 75 80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
85 90 95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100 105 110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115 120 125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130 135 140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145 150 155 160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165 170 175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180 185 190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195 200 205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210 215 220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225 230 235 240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270

Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
275 280 285

Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
290 295 300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305 310 315 320

Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
325 330 335

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
340 345 350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
355 360 365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
370 375 380 385 390 395 400

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
405 410 415

Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
420 425 430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
435 440 445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
450 455 460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
 995 1000 1005

 Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu
 1010 1015 1020

 Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu
 1025 1030 1035 1040

 Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
 1045 1050 1055

 Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
 1060 1065 1070

 Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
 1075 1080 1085

 Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
 1090 1095 1100

 Leu Leu His Leu Met Gly Met
 1105 1110

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligomer primers"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCGCAGAG TGAGAACCAAC 20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligomer primers"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGTATTCT GCAGAGCTGC 20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCCCTTCCCCTACCTTGTG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGAAGCCTGGCAGACAT

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Gly Thr Cys Thr Thr Ala Thr Ala Gly Gly Gly Ala Gly Gly
1 5 10 15

Thr Thr Gly Gly Cys Cys Ala Gly Thr Cys Ala Ala Thr Ala Gly Gly
20 25 30

Thr Thr Ala Cys Thr Thr Ala Thr Gly Ala Gly Thr Thr Gly Cys
35 40 45

Thr Ala Ala Cys Cys Cys Thr Gly Gly Thr Gly Ala Gly Cys Ala Gly
50 55 60

Gly Ala Ala Gly Thr Thr Ala Thr Gly Thr Gly Gly Ala Cys Cys Ala
65 70 75 80

Gly Gly Ala Gly Ala Gly Ala Ala Cys Cys Cys Thr Thr Gly Gly
85 90 95

Thr Thr Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Ala Ala Ala Gly
100 105 110

Gly Ala Gly Ala Gly Gly Thr Thr Gly Ala Cys Cys Cys Thr Ala Ala
115 120 125

Ala Cys Thr Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Ala Gly
130 135 140

Gly Ala Cys Cys Cys Thr Gly Thr Thr Gly Thr Gly Ala Cys Thr Cys
145 150 155 160

Thr Cys Cys Gly Ala Cys Thr Gly Ala Cys Thr Thr Gly Thr Cys Thr
165 170 175

Thr Cys Cys Thr Thr Gly Ala Thr Gly Thr Cys Cys Thr Thr Ala
180 185 190

Ala Gly Cys Cys Gly Gly Ala Gly Cys Thr Gly Ala Thr Thr Cys Gly
195 200 205

Gly Gly Cys Thr Gly Cys Thr Gly Cys Cys Thr Thr Ala Thr Thr Thr
210 215 220

Cys Thr Gly Ala Gly Thr Thr Ala Gly Cys Gly Cys Thr Cys Thr Thr
225 230 235 240

Ala Ala Gly Ala Thr Thr Gly Gly Cys Cys Thr Cys Cys Ala
245 250 255

Gly Thr Thr Thr Gly Ala Gly Gly Ala Ala Gly Gly Gly Cys Gly
260 265 270

Gly Gly Cys Thr Gly Cys Thr Gly Thr Cys Thr Ala Cys Cys Thr Cys
275 280 285

Thr Gly Thr Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
290 295 300

Ala Cys Cys Ala Cys Cys Cys Cys Gly Gly Gly Ala Gly Ala Gly Ala
305 310 315 320

Ala Gly Gly Ala Gly Gly Cys Thr Cys Cys Gly Gly Gly Ala
325 330 335

Ala Thr Cys Thr Cys Gly Cys Ala Cys Ala Thr Thr Cys Cys Ala Gly
340 345 350

Gly Cys Ala Ala Ala Gly Gly Cys Thr Cys Cys Cys Gly Gly Gly Cys
355 360 365

Cys Gly Cys Ala Gly Cys Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala
370 375 380

Cys Ala Cys Cys Cys Thr Thr Gly Gly Cys Cys Cys Gly Gly Gly Cys
385 390 395 400

Cys Ala Gly Gly Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Cys Cys
405 410 415

Thr Cys Gly Cys Thr Gly Cys Gly Ala Gly Gly Gly Gly Ala Gly
420 425 430

Cys Gly Gly Gly Cys Gly Gly Cys Thr Gly Cys Gly Gly Gly Ala
435 440 445

Gly Cys Gly Ala Thr Thr Thr Cys Cys Ala Gly Cys Cys Cys Gly
450 455 460

Gly Thr Thr Thr Gly Thr Gly Cys Thr Cys Thr Gly Thr Gly Thr Gly
465 470 475 480

Thr Thr Thr Gly Thr Cys Thr Gly Cys Cys Thr Cys Thr Gly Gly Ala
485 490 495

Gly Gly Gly Cys Thr Gly Gly Thr Cys Cys Thr Cys Cys Thr Thr
500 505 510

Ala Thr Thr Cys Ala Cys Ala Gly Gly Thr Gly Ala Gly Thr Cys Ala
515 520 525

Cys Ala Cys Cys Cys Thr Gly Ala Ala Ala Cys Ala Cys Ala Gly Gly
530 535 540

Cys Thr Cys Thr Cys Thr Thr Cys Cys Thr Gly Thr Cys Ala Gly Gly
545 550 555 560

Ala Cys Thr Gly Ala Gly Thr Cys Ala Gly Gly Thr Ala Gly Ala Ala
565 570 575

Gly Ala Gly Thr Cys Gly Ala Thr Ala Ala Ala Ala Cys Cys Ala Cys
580 585 590

Cys Thr Gly Ala Thr Cys Ala Ala Gly Gly Ala Ala Ala Gly Gly
595 600 605

Ala Ala Gly Gly Cys Ala Cys Ala Gly Cys Gly Gly Ala Gly Cys Gly
610 615 620

Cys Ala Gly Ala Gly Thr Gly Ala Gly Ala Ala Cys Cys Ala Cys Cys
625 630 635 640

Ala Ala Cys Cys Gly Ala Gly Gly Cys Gly Cys Cys Gly Gly Cys
645 650 655

Ala Gly Cys Gly Ala Cys Cys Cys Thr Gly Cys Ala Gly Cys Gly
660 665 670

Gly Ala Gly Ala Cys Ala Gly Ala Gly Ala Cys Thr Gly Ala Gly Cys
675 680 685

Gly Gly Cys Cys Cys Gly Gly Cys Ala Cys Cys Gly Cys Cys Ala Thr
690 695 700

Gly Cys Cys Thr Gly Cys Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly
705 710 715 720